



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: _____ :
 Doetsch et al. : Group Art Unit: 1645
 Serial No. 09/724,296 : Examiner: Not yet assigned
 Filed: November 28, 2000
 For: BROAD SPECIFICITY DNA DAMAGE ENDONUCLEASE

STATEMENT UNDER 37 C.F.R. §1.821-824

Assistant Commissioner for Patents
 Box Missing Parts
 Washington, D.C. 20231

Sir:

The above-identified patent application contains sequences as defined in 37 C.F.R. §1.821(a). Accordingly, the specification includes a paper copy of Sequence Listing as pages 1 - 36. Applicants also submit a write-protected diskette copy of the Sequence Listing in computer-readable form as required by 37 C.F.R. §1.821(e). All of the sequences now presented in the Sequence Listing are found in the as-filed application. Accordingly, the present Sequence Listing does not constitute the addition of new matter.

In compliance with 37 C.F.R. §1.821(f), the undersigned states that the content of the paper copies and computer-readable copies of the Sequence Listing are the same.

Respectfully submitted,

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 Reg. No. 33,878

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Attorney Docket No.: 25-98A
 bmk: May 17, 2001

CERTIFICATE OF MAILING	
I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C., 20231	
<u>17 May 2001</u> Date	<u>B. Kroge</u> B. Kroge

09/24/2001 09:24:26

#4



SEQUENCE LISTING

<110> Boetsch, Paul W.
Avery, Angela M.
Kaur, Balveen

<120> Broad Specificity DNA Damage Endonuclease

<130> 25-98A

<140> US/09/724,296

<141> 2000-11-28

<150> US/09/327,984

<151> 1999-06-08

<150> US/60/088,521

<151> 1998-06-08

<150> US/60/134,752

<151> 1999-05-18

<160> 71

<170> PatentIn Ver. 2.0

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<211> 2492

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Coding
sequence for fusion protein of GST signal peptide
and the UVDE protein of Schizosaccharomyces pombe

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tattgatggg gatgttaaata taacacagtc tatggccatc atacgttata tagctgacaa 240
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gggaattaca cagaagcaac attactcaga atcggctgat ccaacggcga tttctgggat 2220
gaaacgacgt gctcactctg ataggtgttt tgactttcca ccgtgtgatc ctacaatgga 2280
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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Fusion protein
of GST leader peptide and Schizosaccharomyces
pombe UVDE

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35 40 45

Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp
50 55 60

Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys
65 70 75 80
His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met
85 90 95
Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala
100 105 110
Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu
115 120 125
Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr
130 135 140
Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala
145 150 155 160
Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro
165 170 175
Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp
180 185 190
Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp
195 200 205
Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp His Leu
210 215 220
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225 230 235 240
Ser Lys Arg Ile Val Phe Thr Ile Leu Lys Gln Lys Ala Phe Lys Gly
245 250 255
Asn His Pro Cys Val Pro Ser Val Cys Thr Ile Thr Tyr Ser Arg Phe
260 265 270
His Cys Leu Pro Asp Thr Leu Lys Ser Leu Leu Pro Met Ser Ser Lys
275 280 285
Thr Thr Leu Ser Met Leu Pro Gln Val Asn Ile Gly Ala Asn Ser Phe
290 295 300
Ser Ala Glu Thr Pro Val Asp Leu Lys Lys Glu Asn Glu Thr Glu Leu
305 310 315 320
Ala Asn Ile Ser Gly Pro His Lys Lys Ser Thr Ser Thr Ser Thr Arg
325 330 335

Lys Arg Ala Arg Ser Ser Lys Lys Lys Ala Thr Asp Ser Val Ser Asp
 340 345 350
 Lys Ile Asp Glu Ser Val Ala Ser Tyr Asp Ser Ser Thr His Leu Arg
 355 360 365
 Arg Ser Ser Arg Ser Lys Lys Pro Val Asn Tyr Asn Ser Ser Ser Glu
 370 375 380
 Ser Glu Ser Glu Glu Gln Ile Ser Lys Ala Thr Lys Lys Val Lys Gln
 385 390 395 400
 Lys Glu Glu Glu Glu Tyr Val Glu Glu Val Asp Glu Lys Ser Leu Lys
 405 410 415
 Asn Glu Ser Ser Ser Asp Glu Phe Glu Pro Val Val Pro Glu Gln Leu
 420 425 430
 Glu Thr Pro Ile Ser Lys Arg Arg Arg Ser Arg Ser Ser Ala Lys Asn
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 450 455 460
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 465 470 475 480
 Tyr Ala Cys Leu Asn Thr Ile Leu Arg Ser Met Lys Glu Arg Val Phe
 485 490 495
 Cys Ser Arg Thr Cys Arg Ile Thr Thr Ile Gln Arg Asp Gly Leu Glu
 500 505 510
 Ser Val Lys Gln Leu Gly Thr Gln Asn Val Leu Asp Leu Ile Lys Leu
 515 520 525
 Val Glu Trp Asn His Asn Phe Gly Ile His Phe Met Arg Val Ser Ser
 530 535 540
 Asp Leu Phe Pro Phe Ala Ser His Ala Lys Tyr Gly Tyr Thr Leu Glu
 545 550 555 560
 Phe Ala Gln Ser His Leu Glu Glu Val Gly Lys Leu Ala Asn Lys Tyr
 565 570 575
 Asn His Arg Leu Thr Met His Pro Gly Gln Tyr Thr Gln Ile Ala Ser
 580 585 590
 Pro Arg Glu Val Val Val Asp Ser Ala Ile Arg Asp Leu Ala Tyr His
 595 600 605

Asp Glu Ile Leu Ser Arg Met Lys Leu Asn Glu Gln Leu Asn Lys Asp
 610 615 620
 Ala Val Leu Ile Ile His Leu Gly Gly Thr Phe Glu Gly Lys Lys Glu
 625 630 635 640
 Thr Leu Asp Arg Phe Arg Lys Asn Tyr Gln Arg Leu Ser Asp Ser Val
 645 650 655
 Lys Ala Arg Leu Val Leu Glu Asn Asp Asp Val Ser Trp Ser Val Gln
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 Asp Leu Leu Pro Leu Cys Gln Glu Leu Asn Ile Pro Leu Val Leu Asp
 675 680 685
 Trp His His His Asn Ile Val Pro Gly Thr Leu Arg Glu Gly Ser Leu
 690 695 700
 Asp Leu Met Pro Leu Ile Pro Thr Ile Arg Glu Thr Trp Thr Arg Lys
 705 710 715 720
 Gly Ile Thr Gln Lys Gln His Tyr Ser Glu Ser Ala Asp Pro Thr Ala
 725 730 735
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 740 745 750
 Pro Pro Cys Asp Pro Thr Met Asp Leu Met Ile Glu Ala Lys Glu Lys
 755 760 765
 Glu Gln Ala Val Phe Glu Leu Cys Arg Arg Tyr Glu Leu Gln Asn Pro
 770 775 780
 Pro Cys Pro Leu Glu Ile Met Gly Pro Glu Tyr Asp Gln Thr Arg Asp
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 <221> misc_feature
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<223> DNA sequence encoding UVDE protein, truncated at amino acid residue 228.

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ggtacgcaaa atgttttaga tttaatcaaa ttggttgagt ggaatcacia ctttggcatt 240
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<212> PRT

<213> Schizosaccharomyces pombe

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<221> VARIANT

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<223> Truncated version of the UVDE protein.

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Ser Met Lys Glu Arg Val Phe Cys Ser Arg Thr Cys Arg Ile Thr Thr
      35              40              45

Ile Gln Arg Asp Gly Leu Glu Ser Val Lys Gln Leu Gly Thr Gln Asn
      50              55              60

Val Leu Asp Leu Ile Lys Leu Val Glu Trp Asn His Asn Phe Gly Ile
      65              70              75              80

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His	Phe	Met	Arg	Val	Ser	Ser	Asp	Leu	Phe	Pro	Phe	Ala	Ser	His	Ala	
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Lys	Tyr	Gly	Tyr	Thr	Leu	Glu	Phe	Ala	Gln	Ser	His	Leu	Glu	Glu	Val	
			100					105					110			
Gly	Lys	Leu	Ala	Asn	Lys	Tyr	Asn	His	Arg	Leu	Thr	Met	His	Pro	Gly	
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Asp Glu Lys
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 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Nucleotide
 sequence encoding fusion protein of GST signal
 peptide and the truncated version of *S. pombe* UVDE
 protein.

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<210> 6
 <211> 600
 <212> PRT
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Fusion protein
 comprising the GST signal peptide and the
 truncated UVDE protein of *S. pombe*.

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 Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
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 His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe
 35 40 45
 Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp
 50 55 60
 Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys
 65 70 75 80
 His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met
 85 90 95
 Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala
 100 105 110
 Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu
 115 120 125
 Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr
 130 135 140
 Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala
 145 150 155 160
 Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro
 165 170 175
 Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp
 180 185 190
 Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp
 195 200 205

Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp His Leu
 210 215 220
 Val Pro Arg Gly Ser Asp Asp His Ala Pro Arg Glu Met Phe Asp Cys
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 Leu Asp Lys Pro Ile Pro Trp Arg Gly Arg Leu Gly Tyr Ala Cys Leu
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 Asn Thr Ile Leu Arg Ser Met Lys Glu Arg Val Phe Cys Ser Arg Thr
 260 265 270
 Cys Arg Ile Thr Thr Ile Gln Arg Asp Gly Leu Glu Ser Val Lys Gln
 275 280 285
 Leu Gly Thr Gln Asn Val Leu Asp Leu Ile Lys Leu Val Glu Trp Asn
 290 295 300
 His Asn Phe Gly Ile His Phe Met Arg Val Ser Ser Asp Leu Phe Pro
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 325 330 335
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 370 375 380
 Ser Arg Met Lys Leu Asn Glu Gln Leu Asn Lys Asp Ala Val Leu Ile
 385 390 395 400
 Ile His Leu Gly Gly Thr Phe Glu Gly Lys Lys Glu Thr Leu Asp Arg
 405 410 415
 Phe Arg Lys Asn Tyr Gln Arg Leu Ser Asp Ser Val Lys Ala Arg Leu
 420 425 430
 Val Leu Glu Asn Asp Asp Val Ser Trp Ser Val Gln Asp Leu Leu Pro
 435 440 445
 Leu Cys Gln Glu Leu Asn Ile Pro Leu Val Leu Asp Trp His His His
 450 455 460
 Asn Ile Val Pro Gly Thr Leu Arg Glu Gly Ser Leu Asp Leu Met Pro
 465 470 475 480

Leu Ile Pro Thr Ile Arg Glu Thr Trp Thr Arg Lys Gly Ile Thr Gln
 485 490 495
 Lys Gln His Tyr Ser Glu Ser Ala Asp Pro Thr Ala Ile Ser Gly Met
 500 505 510
 Lys Arg Arg Ala His Ser Asp Arg Val Phe Asp Phe Pro Pro Cys Asp
 515 520 525
 Pro Thr Met Asp Leu Met Ile Glu Ala Lys Glu Lys Glu Gln Ala Val
 530 535 540
 Phe Glu Leu Cys Arg Arg Tyr Glu Leu Gln Asn Pro Pro Cys Pro Leu
 545 550 555 560
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<210> 7

<211> 688

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence encoding GST signal peptide.

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 gcacaacatg ttggttgggt gtccaaaaga gcgtgcagag atttcaatgc ttgaaggagc 300
 ggttttggat attagatacg gtgtttcgag aattgcatat agtaaagact ttgaaactct 360
 caaagttgat tttcttagca agctacctga aatgctgaaa atgttcgaag atcgtttatg 420
 tcataaaaca tattttaaata ttgaccatgt aaccatcct gacttcatgt tgtatgacgc 480
 tcttgatggt gttttataca tggacccaat gtgcctggat gcgttcccaa aattagtttg 540
 ttttaaaaaa cgtattgaag ctatcccaca aattgataag tacttgaaat ccagcaagta 600
 tatagcatgg cctttgcagg gctggcaagc cacgtttggt ggtggcgacc atoctccaaa 660
 atcgatcat ctggttcgcg gtggatcc 688

<210> 8

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid
sequence of GST signal peptide

<400> 8

Met Thr Lys Leu Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val
1 5 10 15

Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
20 25 30

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe
35 40 45

Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp
50 55 60

Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys
65 70 75 80

His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met
85 90 95

Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala
100 105 110

Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu
115 120 125

Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr
130 135 140

Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala
145 150 155 160

Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro
165 170 175

Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp
180 185 190

Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp
195 200 205

Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp His Leu
210 215 220

Val Pro Arg Gly Ser
225

<210> 9
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 9
 tgaggatcca atcgttttca ttttttaatg cttagg 36

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 10
 ggccatgggtt atttttcac ctc 23

<210> 11
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 11
 aatgggatcc gatgatcatg ctccacga 28

<210> 12
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 12
 gggatcctta tttttcatcc tcttctac 28

<210> 13
 <211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing cis-syn
cyclobutane pyrimidine dimer.

<220>
<221> misc_feature
<222> (15)..(16)
<223> At positions 15- 16, the T-T is in the form of
cis-syn cyclobutane pyrimidine dimer.

<400> 13
catgcctgca cgaattaagc aattcgtaat 30

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Undamaged
double stranded oligonucleotide.

<400> 14
catgcctgca cgaattaagc aattcgtaat 30

<210> 15
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing cis-syn
cyclobutane dimer at positions 21-22.

<400> 15
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 16
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing cis-syn
cyclobutane pyrimidine dimer at positions 21-22.

<400> 16
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 17
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing trans- syn 11
cyclobutane pyrimidine dimer at positions 21-22.

<400> 17
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 18
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing a 6-4 photo
product at position 21-22.

<400> 18
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 19
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing a Dewar
isomer.

<400> 19
agctaccatg cctgcacgaa ttaagcaatt cgtaatcatg gtcatagct 49

<210> 20
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide containing cisplatin DNA
diadduct at position 16-17.

<400> 20
 tccctccttc cttccggccc tccttccct tc 32

<210> 21
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n is uracil at
 position 21.

<220>
 <221> misc_feature
 <222> (21)
 <223> The n at position 21 is uracil.

<400> 21
 cttggactgg atgtcggcac nagcggatac aggagca 37

<210> 22
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n is
 dihydrouracil at position 21.

<220>
 <221> misc_feature
 <222> (21)
 <223> At position 21, n is dihydrouracil.

<400> 22
 cttggactgg atgtcggcac nagcggatac aggagca 37

<210> 23
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n at position 21
 represents an abasic site.

<220>
 <221> misc_feature

<222> (21)
 <223> At position 21, n is an abasic site.

 <400> 23
 cttggactgg atgtcggcac nagcggatac aggagca 37

 <210> 24
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n at position 13
 is an inosine.

 <220>
 <221> misc_feature
 <222> (13)
 <223> At position 13, n is inosine.

 <400> 24
 tgcaggtcga ctnaggagga tccccgggta c 31

 <210> 25
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n at position 13
 is xanthine.

 <220>
 <221> misc_feature
 <222> (13)
 <223> N at position 13 is xanthine.

 <400> 25
 tgcaggtcga ctnaggagga tccccgggta c 31

 <210> 26
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Double
 stranded oligonucleotide wherein n at position 21
 is 8-oxoguanine.

<220>
 <221> misc_feature
 <222> (21)
 <223> N at position 21 is 8-oxoguanine.

<400> 26
 cttggactgg atgtcggcac nagcggatac aggagca

37

<210> 27
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double stranded oligonucleotide representing all 16 possible base pair mismatches at position 18 in individual preparations.

<220>
 <221> misc_feature
 <222> (18)
 <223> N at position 18 represents all 16 possible base pair mismatches.

<400> 27
 gtaccocgggg atcctccnag tcgacctgca

30

<210> 28
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Double stranded oligonucleotide containing a CA mismatched base pair at position 21.

<220>
 <221> misc_feature
 <222> (21)
 <223> N at position 21 represents C of C/A mismatched base pair.

<400> 28
 cgttagcatg cctgcacgaa ntaagcaatt cgtaatgcat t

41

<210> 29
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide wherein there is a C/A
mismatched base pair at position 36.

<220>
<221> misc_feature
<222> (36)
<223> N at position 36 represents a C/A mismatched base
pair.

<400> 29
cgttacaagt ccgtcacgaa ttaagcaatt cgtaangcat t

41

<210> 30
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide wherein n at position 31
represents a C/A mismatched base pair.

<220>
<221> misc_feature
<222> (31)
<223> The n at position 31 represents C of C/A
mismatched base pair.

<400> 30
cgttacaagt ccgtcacgaa ttaagcaatt ngtaacgcat t

41

<210> 31
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Double
stranded oligonucleotide wherein n at position 26
is a C/A mismatched base pair.

<220>
<221> misc_feature
<222> (26)
<223> N at position 26 represents a C/A mismatched base
pair.

<400> 31
cgttacaagt ccgtcacgaa ttaagnaatt cgtaacgcat t

41

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<220>
<221> misc_feature
<222> (21)
<223> The n at position 21 represents a C/A mismatched
      base pair.
```

```
<210> 33
<211> 41
<212> DNA
<213> Artificial Sequence
```

```
<220>
<221> misc_feature
<222> (15)
<223> The n at position 15 represents a C/A mismatched
      base pair.
```

```
<210> 34
<211> 41
<212> DNA
<213> Artificial Sequence
```

```
<220>  
<221> misc_feature  
<222> (10)
```

<223> The n at position 10 represents a C/A mismatched base pair.

<400> 34

cggtacaagn ccgtcacgaa ttaagcaatt cgtaacgcat t

41

<210> 35

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Double stranded oligonucleotide wherein n at position 5 is a C/A mismatched base pair.

<220>

<221> misc_feature

<222> (5)

<223> The n at position 5 represents a C/A mismatched base pair.

<400> 35

cggttncaagt ccgtcacgaa ttaagcaatt cgtaacgcat t

41

<210> 36

<211> 656

<212> PRT

<213> Neurospora crassa

<400> 36

Met	Pro	Ser	Arg	Lys	Ser	Lys	Ala	Ala	Ala	Leu	Asp	Thr	Pro	Gln	Ser
1				5					10					15	

Glu	Ser	Ser	Thr	Phe	Ser	Ser	Thr	Leu	Asp	Ser	Ser	Ala	Pro	Ser	Pro
			20					25					30		

Ala	Arg	Asn	Leu	Arg	Arg	Ser	Gly	Arg	Asn	Ile	Leu	Gln	Pro	Ser	Ser
		35					40					45			

Glu	Lys	Asp	Arg	Asp	His	Glu	Lys	Arg	Ser	Gly	Glu	Glu	Leu	Ala	Gly
	50						55				60				

Arg	Met	Met	Gly	Lys	Asp	Ala	Asn	Gly	His	Cys	Leu	Arg	Glu	Gly	Lys
	65				70					75					80

Glu	Gln	Glu	Glu	Gly	Val	Lys	Met	Ala	Ile	Glu	Gly	Leu	Ala	Arg	Met
				85					90					95	

Glu	Arg	Arg	Leu	Gln	Arg	Ala	Thr	Lys	Arg	Gln	Lys	Lys	Gln	Leu	Glu
			100					105					110		

Glu Asp Gly Ile Pro Val Pro Ser Val Val Ser Arg Phe Pro Thr Ala
 115 120 125
 Pro Tyr His His Lys Ser Thr Asn Ala Glu Glu Arg Glu Ala Lys Glu
 130 135 140
 Pro Val Leu Lys Thr His Ser Lys Asp Val Glu Arg Glu Ala Glu Ile
 145 150 155 160
 Gly Val Asp Asp Val Val Lys Met Glu Pro Ala Ala Thr Asn Ile Ile
 165 170 175
 Glu Pro Glu Asp Ala Gln Asp Ala Ala Glu Arg Gly Ala Ala Arg Pro
 180 185 190
 Pro Ala Val Asn Ser Ser Tyr Leu Pro Leu Pro Trp Lys Gly Arg Leu
 195 200 205
 Gly Tyr Ala Cys Leu Asn Thr Tyr Leu Arg Asn Ala Lys Pro Pro Ile
 210 215 220
 Phe Ser Ser Arg Thr Cys Arg Met Ala Ser Ile Val Asp His Arg His
 225 230 235 240
 Pro Leu Gln Phe Glu Asp Glu Pro Glu His His Leu Lys Asn Lys Pro
 245 250 255
 Asp Lys Ser Lys Glu Pro Gln Asp Glu Leu Gly His Lys Phe Val Gln
 260 265 270
 Glu Leu Gly Leu Ala Asn Ala Arg Asp Ile Val Lys Met Leu Cys Trp
 275 280 285
 Asn Glu Lys Tyr Gly Ile Arg Phe Leu Arg Leu Ser Ser Glu Met Phe
 290 295 300
 Pro Phe Ala Ser His Pro Val His Gly Tyr Lys Leu Ala Pro Phe Ala
 305 310 315 320
 Ser Glu Val Leu Ala Glu Ala Gly Arg Val Ala Ala Glu Leu Gly His
 325 330 335
 Arg Leu Thr Thr His Pro Gly Gln Phe Thr Gln Leu Gly Ser Pro Arg
 340 345 350
 Lys Glu Val Val Glu Ser Ala Ile Arg Asp Leu Glu Tyr His Asp Glu
 355 360 365
 Leu Leu Ser Leu Leu Lys Leu Pro Glu Gln Gln Asn Arg Asp Ala Val
 370 375 380

Met Ile Ile His Met Gly Gly Gln Phe Gly Asp Lys Ala Ala Thr Leu
 385 390 395 400
 Glu Arg Phe Lys Arg Asn Tyr Ala Arg Leu Ser Gln Ser Cys Lys Asn
 405 410 415
 Arg Leu Val Leu Glu Asn Asp Asp Val Gly Trp Thr Val His Asp Leu
 420 425 430
 Leu Pro Val Cys Glu Glu Leu Asn Ile Pro Met Val Leu Asp Tyr His
 435 440 445
 His His Asn Ile Cys Phe Asp Pro Ala His Leu Arg Glu Gly Thr Leu
 450 455 460
 Asp Ile Ser Asp Pro Lys Leu Gln Glu Arg Ile Ala Asn Thr Trp Lys
 465 470 475 480
 Arg Lys Gly Ile Lys Gln Lys Met His Tyr Ser Glu Pro Cys Asp Gly
 485 490 495
 Ala Val Thr Pro Arg Asp Arg Arg Lys His Arg Pro Arg Val Met Thr
 500 505 510
 Leu Pro Pro Cys Pro Pro Asp Met Asp Leu Met Ile Glu Ala Lys Asp
 515 520 525
 Lys Glu Gln Ala Val Phe Glu Leu Met Arg Thr Phe Lys Leu Pro Gly
 530 535 540
 Phe Glu Lys Ile Asn Asp Met Val Pro Tyr Asp Arg Asp Asp Glu Asn
 545 550 555 560
 Arg Pro Ala Pro Pro Val Lys Ala Pro Lys Lys Lys Lys Gly Gly Lys
 565 570 575
 Arg Lys Arg Thr Thr Asp Glu Glu Ala Ala Glu Pro Glu Glu Val Asp
 580 585 590
 Thr Ala Ala Asp Asp Val Lys Asp Ala Pro Glu Gly Pro Lys Glu Val
 595 600 605
 Pro Glu Glu Glu Arg Ala Met Gly Gly Pro Tyr Asn Arg Val Tyr Trp
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 Pro Leu Gly Cys Glu Glu Trp Leu Lys Pro Lys Lys Arg Glu Val Lys
 625 630 635 640
 Lys Gly Lys Val Pro Glu Glu Val Glu Asp Glu Gly Glu Phe Asp Gly
 645 650 655

<210> 37
 <211> 317
 <212> PRT
 <213> Bacillus subtilis

<400> 37

Met	Ile	Phe	Arg	Phe	Gly	Phe	Val	Ser	Asn	Ala	Met	Ser	Leu	Trp	Asp
1				5					10					15	
Ala	Ser	Pro	Ala	Lys	Thr	Leu	Thr	Phe	Ala	Arg	Tyr	Ser	Lys	Leu	Ser
			20					25					30		
Lys	Thr	Glu	Arg	Lys	Glu	Ala	Leu	Leu	Thr	Val	Thr	Lys	Ala	Asn	Leu
		35					40					45			
Arg	Asn	Thr	Met	Arg	Thr	Leu	His	Tyr	Ile	Ile	Gly	His	Gly	Ile	Pro
	50					55					60				
Leu	Tyr	Arg	Phe	Ser	Ser	Ser	Ile	Val	Pro	Leu	Ala	Thr	His	Pro	Asp
65					70					75					80
Val	Met	Trp	Asp	Phe	Val	Thr	Pro	Phe	Gln	Lys	Glu	Phe	Arg	Glu	Ile
				85					90					95	
Gly	Glu	Leu	Val	Lys	Thr	His	Gln	Leu	Arg	Thr	Ser	Phe	His	Pro	Asn
		100						105					110		
Gln	Phe	Thr	Leu	Phe	Thr	Ser	Pro	Lys	Glu	Ser	Val	Thr	Lys	Asn	Ala
	115						120					125			
Val	Thr	Asp	Met	Ala	Tyr	His	Tyr	Arg	Met	Leu	Glu	Ala	Met	Gly	Ile
	130					135					140				
Ala	Asp	Arg	Ser	Val	Ile	Asn	Ile	His	Ile	Gly	Gly	Ala	Tyr	Gly	Asn
145					150					155					160
Lys	Asp	Thr	Ala	Thr	Ala	Gln	Phe	His	Gln	Asn	Ile	Lys	Gln	Leu	Pro
			165						170					175	
Gln	Glu	Ile	Lys	Glu	Arg	Met	Thr	Leu	Glu	Asn	Asp	Asp	Lys	Thr	Tyr
		180						185					190		
Thr	Thr	Glu	Glu	Thr	Leu	Gln	Val	Cys	Glu	Gln	Glu	Asp	Val	Pro	Phe
	195						200					205			
Val	Phe	Asp	Phe	His	His	Phe	Tyr	Ala	Asn	Pro	Asp	Asp	His	Ala	Asp
	210					215					220				

Leu Asn Val Ala Leu Pro Arg Met Ile Lys Thr Trp Glu Arg Ile Gly
 225 230 235 240
 Leu Gln Pro Lys Val His Leu Ser Ser Pro Lys Ser Glu Gln Ala Ile
 245 250 255
 Arg Ser His Ala Asp Tyr Val Asp Ala Asn Phe Leu Leu Glu Arg Phe
 260 265 270
 Arg Gln Trp Gly Thr Asn Ile Asp Phe Met Ile Glu Ala Lys Gln Lys
 275 280 285
 Asp Lys Ala Leu Leu Arg Leu Met Asp Glu Leu Ser Ser Ile Arg Gly
 290 295 300
 Val Lys Arg Ile Gly Gly Gly Ala Leu Gln Trp Lys Ser
 305 310 315

<210> 38
 <211> 580
 <212> PRT
 <213> Homo sapiens

<400> 38
 Met Gly Thr Thr Gly Leu Glu Ser Leu Ser Leu Gly Asp Arg Gly Ala
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 Ala Pro Thr Val Thr Ser Ser Glu Arg Leu Val Pro Asp Pro Pro Asn
 20 25 30
 Asp Leu Arg Lys Glu Asp Val Ala Met Glu Leu Glu Arg Val Gly Glu
 35 40 45
 Asp Glu Glu Gln Met Met Ile Lys Arg Ser Ser Glu Cys Asn Pro Leu
 50 55 60
 Leu Gln Glu Pro Ile Ala Ser Ala Gln Phe Gly Ala Thr Ala Gly Thr
 65 70 75 80
 Glu Cys Arg Lys Ser Val Pro Cys Gly Trp Glu Arg Val Val Lys Gln
 85 90 95
 Arg Leu Phe Gly Lys Thr Ala Gly Arg Phe Asp Val Tyr Phe Ile Ser
 100 105 110
 Pro Gln Gly Leu Lys Phe Arg Ser Lys Ser Ser Leu Ala Asn Tyr Leu
 115 120 125
 His Lys Asn Gly Glu Thr Ser Leu Lys Pro Glu Asp Phe Asp Phe Thr
 130 135 140

Val	Leu	Ser	Lys	Arg	Gly	Ile	Lys	Ser	Arg	Tyr	Lys	Asp	Cys	Ser	Met	
145					150					155					160	
Ala	Ala	Leu	Thr	Ser	His	Leu	Gln	Asn	Gln	Ser	Asn	Asn	Ser	Asn	Trp	
				165					170						175	
Asn	Leu	Arg	Thr	Arg	Ser	Lys	Cys	Lys	Lys	Asp	Val	Phe	Met	Pro	Pro	
			180					185					190			
Ser	Ser	Ser	Ser	Glu	Leu	Gln	Glu	Ser	Arg	Gly	Leu	Ser	Asn	Phe	Thr	
		195					200					205				
Ser	Thr	His	Leu	Leu	Leu	Lys	Glu	Asp	Glu	Gly	Val	Asp	Asp	Val	Asn	
	210					215					220					
Phe	Arg	Lys	Val	Arg	Lys	Pro	Lys	Gly	Lys	Val	Thr	Ile	Leu	Lys	Gly	
225					230					235					240	
Ile	Pro	Ile	Lys	Lys	Thr	Lys	Lys	Gly	Cys	Arg	Lys	Ser	Cys	Ser	Gly	
			245					250						255		
Phe	Val	Gln	Ser	Asp	Ser	Lys	Arg	Glu	Ser	Val	Cys	Asn	Lys	Ala	Asp	
		260						265					270			
Ala	Glu	Ser	Glu	Pro	Val	Ala	Gln	Lys	Ser	Gln	Leu	Asp	Arg	Thr	Val	
	275						280					285				
Cys	Ile	Ser	Asp	Ala	Gly	Ala	Cys	Gly	Glu	Thr	Leu	Ser	Val	Thr	Ser	
	290					295					300					
Glu	Glu	Asn	Ser	Leu	Val	Lys	Lys	Lys	Glu	Arg	Ser	Leu	Ser	Ser	Gly	
305				310					315						320	
Ser	Asn	Phe	Cys	Ser	Glu	Gln	Lys	Thr	Ser	Gly	Ile	Ile	Asn	Lys	Phe	
			325					330						335		
Cys	Ser	Ala	Lys	Asp	Ser	Glu	His	Asn	Glu	Lys	Tyr	Glu	Asp	Thr	Phe	
		340						345					350			
Leu	Glu	Ser	Glu	Glu	Ile	Gly	Thr	Lys	Val	Glu	Val	Val	Glu	Arg	Lys	
	355					360						365				
Glu	His	Leu	His	Thr	Asp	Ile	Leu	Lys	Arg	Gly	Ser	Glu	Met	Asp	Asn	
	370					375					380					
Asn	Cys	Ser	Pro	Thr	Arg	Lys	Asp	Phe	Thr	Gly	Glu	Lys	Ile	Phe	Gln	
385					390					395					400	
Glu	Asp	Thr	Ile	Pro	Arg	Thr	Gln	Ile	Glu	Arg	Arg	Lys	Thr	Ser	Leu	
			405					410						415		

Tyr Phe Ser Ser Lys Tyr Asn Lys Glu Ala Leu Ser Pro Pro Arg Arg
 420 425 430

Lys Ala Phe Lys Lys Trp Thr Pro Pro Arg Ser Pro Phe Asn Leu Val
 435 440 445

Gln Glu Thr Leu Phe His Asp Pro Trp Lys Leu Leu Ile Ala Thr Ile
 450 455 460

Phe Leu Asn Arg Thr Ser Gly Lys Met Ala Ile Pro Val Leu Trp Lys
 465 470 475 480

Phe Leu Glu Lys Tyr Pro Ser Ala Glu Val Ala Arg Thr Ala Asp Trp
 485 490 495

Arg Asp Val Ser Glu Leu Leu Lys Pro Leu Gly Leu Tyr Asp Leu Arg
 500 505 510

Ala Lys Thr Ile Val Lys Phe Ser Asp Glu Tyr Leu Thr Lys Gln Trp
 515 520 525

Lys Tyr Pro Ile Glu Leu His Gly Ile Gly Lys Tyr Gly Asn Asp Ser
 530 535 540

Tyr Arg Ile Phe Cys Val Asn Glu Trp Lys Gln Val His Pro Glu Asp
 545 550 555 560

His Lys Leu Asn Lys Tyr His Asp Trp Leu Trp Glu Asn His Glu Lys
 565 570 575

Leu Ser Leu Ser
 580

<210> 39

<211> 294

<212> PRT

<213> Deinococcus radiodurans

<400> 39

Gln Leu Gly Leu Val Cys Leu Thr Val Gly Pro Glu Val Arg Phe Arg
 1 5 10 15

Thr Val Thr Leu Ser Arg Tyr Arg Ala Leu Ser Pro Ala Glu Arg Glu
 20 25 30

Ala Lys Leu Leu Asp Leu Tyr Ser Ser Asn Ile Lys Thr Leu Arg Gly
 35 40 45

Ala Ala Asp Tyr Cys Ala Ala His Asp Ile Arg Leu Tyr Arg Leu Ser
 50 55 60

Ser Ser Leu Phe Pro Met Leu Asp Leu Ala Gly Asp Asp Thr Gly Ala
 65 70 75 80
 Ala Val Leu Thr His Leu Ala Pro Gln Leu Leu Glu Ala Gly His Ala
 85 90 95
 Phe Thr Asp Ala Gly Val Arg Leu Leu Met His Pro Glu Gln Phe Ile
 100 105 110
 Val Leu Asn Ser Asp Arg Pro Glu Val Arg Glu Ser Ser Val Arg Ala
 115 120 125
 Met Ser Ala His Ala Arg Val Met Asp Gly Leu Gly Leu Ala Arg Thr
 130 135 140
 Pro Trp Asn Leu Leu Leu Leu His Gly Gly Lys Gly Gly Arg Gly Ala
 145 150 155 160
 Glu Leu Ala Ala Leu Ile Pro Asp Leu Pro Asp Pro Val Arg Leu Arg
 165 170 175
 Leu Gly Leu Glu Asn Asp Glu Arg Ala Tyr Ser Pro Ala Glu Leu Leu
 180 185 190
 Pro Ile Cys Glu Ala Thr Gly Thr Pro Leu Val Phe Asp Ala His His
 195 200 205
 His Val Val His Asp Lys Leu Pro Asp Gln Glu Asp Pro Ser Val Arg
 210 215 220
 Glu Trp Val Leu Arg Ala Arg Ala Thr Trp Gln Pro Pro Glu Trp Gln
 225 230 235 240
 Val Val His Leu Ser Asn Gly Ile Glu Gly Pro Gln Asp Arg Arg His
 245 250 255
 Ser His Leu Ile Ala Asp Phe Pro Ser Ala Tyr Ala Asp Val Pro Gln
 260 265 270
 Ile Glu Val Glu Ala Lys Gly Lys Glu Glu Ala Ile Ala Ala Leu Arg
 275 280 285
 Leu Met Ala Pro Phe Lys
 290

<210> 40

<211> 39

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 40
 cacagactcc ctctgtcata ggtttgagtt tatatggaa 39

<210> 41
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 41
 ttccatataa actcaaacct atgacagagg gagtctgtg 39

<210> 42
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 42
 cacagactcc ctctgtcata ggttcatgag tttatatgga a 41

<210> 43
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 43
 cacagactcc ctctgtcata ggttcacatg agtttatatg gaa 43

<210> 44
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 44
cacagactcc ctctgtcata gggtcacaca tgagtttata tggaa 45

<210> 45
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 45
cacagactcc ctctgtcata gggtcacaca catgagttta tatggaa 47

<210> 46
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 46
cacagactcc ctctgtcata gggtgagtac tagtactctg agtttatatg gaa 53

<210> 47
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 47
cgttagaact ccgtcacgaa ttaagcaatt agtaatgcat t 41

<210> 48
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 48
aatgcattac taattgctta attcgtgacg gagttctaac g 41

<210> 49
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 49
cgttagaact ccgtcacgaa ttaagcaatt caagtaatgc att 43

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 50
cgttagaact ccgtcacgaa ttaagcaatt cacaagtaat gcatt 45

<210> 51
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 51
cgttagaact ccgtcacgaa ttaagcaatt cacacaagta atgcatt 47

<210> 52
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 52
cgttagaact ccgtcacgaa ttaagcaatt cacacacaag taatgcatt 49

<210> 53
<211> 41
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 53

cgttacaagt ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 54

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 54

aatgcattac gaattgctta attcgtgacg gacttgtaac g 41

<210> 55

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 55

cgttacaagt ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 56

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 56

aatgcgttac aaattgctta attcgtgacg gacttgtaac g 41

<210> 57

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 57

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<210> 58

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 58

aatgcgttac gaattactta attcgtgacg gacttgtaac g 41

<210> 59

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 59

cgttacaagt ccgtcacgac ttaagcaatt cgtaacgcat t 41

<210> 60

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 60

aatgcgttac gaattgctta aatcgtgacg gacttgtaac g 41

<210> 61

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 61
 cggtacaagt ccgtcacgaa ttaagcaatt cgtaacgcat t 41

 <210> 62
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

 <400> 62
 aatgcgttac gaattgctta attcgtaacg gacttgtaac g 41

 <210> 63
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

 <400> 63
 cgttacaagc ccgtcacgaa ttaagcaatt cgtaacgcat t 41

 <210> 64
 <211> 41
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

 <400> 64
 aatgcgttac gaattgctta attcgtgacg gacttgtaac g 41

 <210> 65
 <211> 41
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

 <400> 65
 cgttccaagt ccgtcacgaa ttaagcaatt cgtaacgcat t 41

<210> 66
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 66
aatgcgttac gaattgctta attcgtgacg gacttgaaac g 41

<210> 67
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 67
tgcacggacc tcgagagaac cgaacgatcc ggatgtgac atgggacaga attcgcacac 60
tgcaactcgac gatagtct 78

<210> 68
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 68
tgcagtgtgc gaattctgtc ccatcatcac atccggatcg ttcggttct 49

<210> 69
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 69
gactatcgtg cagtgcagtg tgcgaattct gtcccatcat cacatccgga tcgttcggtt 60
ct 62

<210> 70

<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 70
tgcagtgtgc gaattctgtc ccatcatcac atccggatcg ttcggttctc tcgaggtccg 60
tgca 64

<210> 71
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 71
gagactatcg tgcagtgcag tgtgcgaatt ctgtcccatc atcacatccg gatcgttcgg 60
ttctctcgag gtccgtgca 79